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10/509247
RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/509,247A
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RAW SEQUENCE LISTING

DATE: 03/22/2005

PATENT APPLICATION: US/10/509,247A

TIME: 09:53:09

Input Set : E:\P023P01.ST25.txt

Output Set: N:\CRF4\03222005\J509247A.raw

3 <110> APPLICANT: Japan Science and Technology Corporation
 4 Kuroda, Shunichi
 5 Tanizawa, Katsuyuki
 6 Kondo, Akihiko
 7 Ueda, Masakazu
 8 Seno, Masaharu
 9 Tada, Hiroko
 11 <120> TITLE OF INVENTION: DRUG CONTAINING HOLLOW PROTEIN NANOPARTICLES OF PARTICLE-
 FORMING
 12 PROTEIN, FUSED WITH DISEASE-TREATING TARGET-CELL-SUBSTANCE
 14 <130> FILE REFERENCE: P023P01/US
 16 <140> CURRENT APPLICATION NUMBER: US 10/509,247A
 17 <141> CURRENT FILING DATE: 2004-09-28
 19 <150> PRIOR APPLICATION NUMBER: PCT/JP03/02602
 20 <151> PRIOR FILING DATE: 2003-03-05
 22 <150> PRIOR APPLICATION NUMBER: JP2002-97280
 23 <151> PRIOR FILING DATE: 2002-03-29
 25 <160> NUMBER OF SEQ ID NOS: 20
 27 <170> SOFTWARE: PatentIn version 3.3
 29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 36
 31 <212> TYPE: DNA
 32 <213> ORGANISM: Artificial Sequence
 34 <220> FEATURE:
 35 <223> OTHER INFORMATION: Artificially Synthesized Sequence
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 43 <212> TYPE: DNA
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 46 <220> FEATURE:
 47 <223> OTHER INFORMATION: Artificially Synthesized Sequence
 49 <400> SEQUENCE: 2
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 53 <210> SEQ ID NO: 3
 54 <211> LENGTH: 28
 55 <212> TYPE: DNA
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 58 <220> FEATURE:
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 62 ataccggtgg gctgtgatct gcctcaga 28
 65 <210> SEQ ID NO: 4

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178 <220> FEATURE:
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183 <221> NAME/KEY: CDS
184 <222> LOCATION: (23)..(1999)
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189                               Met Arg Ser Leu Leu Ile Leu Val Leu Cys
190                               1           5           10
192 ttc ttg cca ttg gct gct ttg ggt aag gtt cga caa ggc atg ggg acg    100
193 Phe Leu Pro Leu Ala Ala Leu Gly Lys Val Arg Gln Gly Met Gly Thr
194                               15           20           25
196 aat ctt tct gtt ccc aat cct ctg gga ttc ttt ccc gat cac cag ttg    148
197 Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu
198                               30           35           40
200 gac cct gcg ttc gga gcc aac tca aac aat cca gat tgg gac ttc aac    196
201 Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn
202                               45           50           55
204 ccc aac aag gat caa tgg cca gag gca aat cag gta gga gcg gga gca    244
205 Pro Asn Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Ala
206                               60           65           70
208 ttc ggg cca ggg ttc acc cca cca cac ggc ggt ctt ttg ggg tgg agc    292

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209	Phe	Gly	Pro	Gly	Phe	Thr	Pro	Pro	His	Gly	Gly	Leu	Leu	Gly	Trp	Ser	
210	75					80					85					90	
212	cct	cag	gct	cag	ggc	ata	ttg	aca	aca	gtg	cca	gca	gca	cct	cct	cct	340
213	Pro	Gln	Ala	Gln	Gly	Ile	Leu	Thr	Thr	Val	Pro	Ala	Ala	Pro	Pro	Pro	
214				95						100					105		
216	gcc	tcc	acc	aat	cgg	cag	tca	gga	aga	cag	cct	act	ccc	atc	tct	cca	388
217	Ala	Ser	Thr	Asn	Arg	Gln	Ser	Gly	Arg	Gln	Pro	Thr	Pro	Ile	Ser	Pro	
218				110					115					120			
220	cct	cta	aga	gac	agt	cat	cct	cag	gcc	atg	cag	tgg	aat	tcc	aca	aca	436
221	Pro	Leu	Arg	Asp	Ser	His	Pro	Gln	Ala	Met	Gln	Trp	Asn	Ser	Thr	Thr	
222			125					130					135				
224	ttc	cac	caa	gct	ctg	cta	gat	ccc	aga	gtg	agg	ggc	cta	tat	ttt	cct	484
225	Phe	His	Gln	Ala	Leu	Leu	Asp	Pro	Arg	Val	Arg	Gly	Leu	Tyr	Phe	Pro	
226		140					145					150					
228	gct	ggt	ggc	tcc	agt	tcc	gga	aca	gta	aac	cct	gtt	ccg	act	act	gcc	532
229	Ala	Gly	Gly	Ser	Ser	Ser	Gly	Thr	Val	Asn	Pro	Val	Pro	Thr	Thr	Ala	
230	155					160				165						170	
232	tca	ccc	ata	tct	ggg	gac	cct	gca	ccg	aac	atg	gag	aac	aca	aca	tca	580
233	Ser	Pro	Ile	Ser	Gly	Asp	Pro	Ala	Pro	Asn	Met	Glu	Asn	Thr	Thr	Ser	
234				175					180						185		
236	gga	ttc	cta	gga	ccc	ctg	ctc	gtg	tta	cag	gcg	ggg	ttt	ttc	ttg	ttg	628
237	Gly	Phe	Leu	Gly	Pro	Leu	Leu	Val	Leu	Gln	Ala	Gly	Phe	Phe	Leu	Leu	
238			190					195					200				
240	aca	aga	atc	ctc	aca	ata	cca	cag	agt	cta	gac	tcg	tgg	tgg	act	tct	676
241	Thr	Arg	Ile	Leu	Thr	Ile	Pro	Gln	Ser	Leu	Asp	Ser	Trp	Trp	Thr	Ser	
242			205					210					215				
244	ctc	aat	ttt	cta	ggg	gga	gca	ccc	acg	tgt	cct	ggc	caa	aat	tcg	cag	724
245	Leu	Asn	Phe	Leu	Gly	Gly	Ala	Pro	Thr	Cys	Pro	Gly	Gln	Asn	Ser	Gln	
246		220				225						230					
248	tcc	cca	acc	tcc	aat	cac	tca	cca	acc	tct	tgt	cct	cca	att	tgt	cct	772
249	Ser	Pro	Thr	Ser	Asn	His	Ser	Pro	Thr	Ser	Cys	Pro	Pro	Ile	Cys	Pro	
250	235					240				245						250	
252	ggc	tat	cgc	tgg	atg	tgt	ctg	cgg	cgt	ttt	atc	ata	ttc	ctc	ttc	atc	820
253	Gly	Tyr	Arg	Trp	Met	Cys	Leu	Arg	Arg	Phe	Ile	Ile	Phe	Leu	Phe	Ile	
254				255					260						265		
256	ctg	ctg	cta	tgc	ctc	atc	ttc	ttg	ttg	gtt	ctt	ctg	gac	tac	caa	ggt	868
257	Leu	Leu	Leu	Cys	Leu	Ile	Phe	Leu	Leu	Val	Leu	Leu	Asp	Tyr	Gln	Gly	
258			270						275					280			
260	atg	ttg	ccc	gtt	tgt	cct	cta	ctt	cca	gga	aca	tca	acc	acc	agc	acg	916
261	Met	Leu	Pro	Val	Cys	Pro	Leu	Leu	Pro	Gly	Thr	Ser	Thr	Thr	Ser	Thr	
262			285					290					295				
264	ggg	cca	tgc	aag	acc	tgc	acg	att	cct	gct	caa	gga	acc	tct	atg	ttt	964
265	Gly	Pro	Cys	Lys	Thr	Cys	Thr	Ile	Pro	Ala	Gln	Gly	Thr	Ser	Met	Phe	
266		300				305						310					
268	ccc	tct	tgt	tgc	tgt	aca	aaa	cct	tcg	gac	gga	aac	tgc	act	tgt	att	1012
269	Pro	Ser	Cys	Cys	Cys	Thr	Lys	Pro	Ser	Asp	Gly	Asn	Cys	Thr	Cys	Ile	
270	315					320				325						330	
272	ccc	atc	cca	tca	tcc	tgg	gct	ttc	gca	aga	ttc	cta	tgg	gag	tgg	gcc	1060
273	Pro	Ile	Pro	Ser	Ser	Trp	Ala	Phe	Ala	Arg	Phe	Leu	Trp	Glu	Trp	Ala	

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274		335		340		345		
276	tca gtc cgt ttc tcc tgg ctc agt tta cta gtg cca ttt gtt cag tgg							1108
277	Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp							
278		350		355		360		
280	ttc gta ggg ctt tcc ccc act gtt tgg ctt tca gtt ata tgg atg atg							1156
281	Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met							
282		365		370		375		
284	tgg tat tgg ggg cca agt ctg tac aac atc ttg agt ccc ttt tta cct							1204
285	Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro							
286		380		385		390		
288	cta tta cca att ttc ttt tgt ctt tgg gta tat att gat tac aag gat							1252
289	Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile Asp Tyr Lys Asp							
290	395		400		405		410	
292	gac gac gat aag ata ccg gtc gcc acc atg gtg agc aag ggc gag gag							1300
293	Asp Asp Asp Lys Ile Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu							
294		415		420		425		
296	ctg ttc acc ggg gtg gtg ccc atc ctg gtc gag ctg gac ggc gac gta							1348
297	Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val							
298		430		435		440		
300	aac ggc cac aag ttc agc gtg tcc ggc gag ggc gag ggc gat gcc acc							1396
301	Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr							
302		445		450		455		
304	tac ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc							1444
305	Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro							
306		460		465		470		
308	gtg ccc tgg ccc acc ctc gtg acc acc ctg acc tac ggc gtg cag tgc							1492
309	Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys							
310	475		480		485		490	
312	ttc agc cgc tac ccc gac cac atg aag cag cac gac ttc ttc aag tcc							1540
313	Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser							
314		495		500		505		
316	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac							1588
317	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp							
318		510		515		520		
320	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc							1636
321	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr							
322		525		530		535		
324	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc							1684
325	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly							
326		540		545		550		
328	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc							1732
329	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val							
330	555		560		565		570	
332	tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag							1780
333	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys							
334		575		580		585		
336	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac							1828
337	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr							
338		590		595		600		

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